

EX. SEARCH NOTES

GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query		Match	Length	DB	ID	Description
No.	Score						

1	18.6	20.0	45	6	AR078468		AR078468
Sequence							
2	17.2	18.5	30	6	AI1493		AI1493
Nucleotide							
3	17	18.3	49	6	AX404630		AX404630
Sequence							
4	16.8	18.1	50	6	AX159154		AX159154
Sequence							
5	16.6	17.8	30	6	AR093240		AR093240
Sequence							
c	16.6	17.8	34	11	C75763		C75763 Homo
sapien							
c	16.6	17.8	39	6	I44807		I44807 Sequence
31							
8	16.6	17.8	49	6	I79331		I79331 Sequence
34							
9	16.6	17.8	50	6	AR125663		AR125663
Sequence							
10	16.6	17.8	50	6	I47075		I47075 Sequence
5							
c	16.4	17.6	47	6	AR149818		AR149818
Sequence							
c	16.4	17.6	47	6	AR289717		AR289717
Sequence							
c	16.4	17.6	47	6	BD007169		BD007169
Improved							
14	16.4	17.6	50	6	AX159152		AX159152
Sequence							
c	16.2	17.4	40	6	AR078049		AR078049
Sequence							

16	16.2	17.4	47	6	AR288877	AR288877		
Sequence	17	16.2	17.4	48	9	HSTCRA2J		
H.sapiens	(Z28346		
alpha	V	16.2	17.4	48	9	S74027		
c	19	16.2	17.4	50	6	AR356512		
Sequence						AR356512		
20	16	17.2	41	6	AX513847	AX513847		
Sequence	c	21	16	17.2	41	6	AX514818	
Sequence	c	22	16	17.2	41	6	AX517176	
Sequence	c	23	16	17.2	41	6	AX517724	
Sequence	c	24	16	17.2	50	6	AX199602	
Sequence	c	25	16	17.2	50	9	AP044111	
sapi						AP044111 Homo		
c	26	15.8	17.0	39	6	BD263040	BD263040	
Vectors	f	c	27	15.8	17.0	40	6	AR127202
Sequence	c	28	15.8	17.0	40	6	BD130543	
Controll	e	c	29	15.8	17.0	42	6	AR109086
Sequence	c	30	15.8	17.0	42	6	AR200741	
Sequence	c	31	15.8	17.0	44	6	I43354	
8						Sequence	I43354 Sequence	
Sequence	c	32	15.8	17.0	47	6	AR289659	AR289659
Sequence	c	33	15.6	16.8	27	6	AX417271	AX417271
Sequence	c	34	15.6	16.8	30	6	BD095102	BD095102 N-Type
ca								
Sequence	c	35	15.6	16.8	33	6	AR022050	AR022050
Sequence	c	36	15.6	16.8	33	6	192840	192840 Sequence
14								
for	c	37	15.6	16.8	35	6	E27408	E27408 Processa
methy	c	38	15.6	16.8	43	6	BD190955	BD190955 DNA
sapi	c	39	15.6	16.8	43	9	F202550S09	AF202558 Homo
Sequence	c	40	15.6	16.8	44	6	AX457962	AX457962
Sequence	c	41	15.6	16.8	47	6	AR284775	AR284775
Sequence	c	42	15.6	16.8	48	6	AX805934	AX805934
Sequence	c	43	15.6	16.8	50	6	AX157284	AX157284
Sequence	c	44	15.4	16.6	25	6	AX609394	AX609394
G p	c	45	15.4	16.6	28	6	BD141779	BD141779 Novel

ALIGNMENTS

JOURNAL these organisms producing the same
 Patent: EP 0170204-A 33 05-FEB-1986;
 BOESRINGER INGELHEIM INTERNATIONAL GmbH

FEATURES
 source 1..30
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORIGIN

Query Match 18.5%; Score 17 2; DB 6; Length 30;
 Best Local Similarity 86.4%; Pred. No. 1.4e+05;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 GGAGCACTCCATTCTGCCCTGGG 28
 Db 9 GGAGGACTCCATTCTGGCTGTG 30

RESULT 3
 AX404630
 LOCUS AX404630 49 bp DNA linear PAT 14-
 JUN-2002
 DEFINITION Sequence 4 from Patent WO0224745.
 ACCESSION AX404630
 VERSION AX404630.1 GI:21437911
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Abken,H. and Schinkoethe,T.
 TITLE Method for detecting tumor cells
 JOURNAL Patent: WO 0224745-A 4 28-MAR-2002;
 Abken, Hinrich (DE)

FEATURES
 source 1..49
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 18.3%; Score 17; DB 6; Length 49;
 Best Local Similarity 63.4%; Pred. No. 1.8e+05;
 Matches 26; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 5 TGGGAGCACTCCATTCTGCCCTGGGTGACAATGCCCTGGTT 45
 Db 2 TGGAAAACCTCCACTCACCTGTTCAAAAGTGGGGTTGGTT 42

RESULT 4
 AX159154
 LOCUS AX159154 50 bp DNA linear PAT 22-
 JUN-2001
 DEFINITION Sequence 2482 from Patent WO0140521.
 ACCESSION AX159154
 VERSION AX159154.1 GI:14540485
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shimkets,R.A. and Leach,M.
 TITLE Nucleic acid containing single nucleotide polymorphisms and
 methods of use thereof
 JOURNAL Patent: WO 0140521-A 2482 07-JUN-2001;
 Curagen Corporation (US)

FEATURES
 source 1..50
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 misc_feature 25..26
 /note="Nucleotide deleted between bases 25 and 26"
 Accession number cg39667412*
 misc_feature 26
 /note="#2 of 2 allelic variants (2481 is other entry)"

ORIGIN

Query Match 18.1%; Score 16.8; DB 6; Length 50;
 Best Local Similarity 61.4%; Pred. No. 2.2e+05;
 Matches 27; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 37 CCTTGGTTCAACACTATCGGAATGTGACTGTGGGCTCCAGA 80
 Db 5 CCATGGGTTGACACAGGGACTGTCAATCACAGGCTTCTATA 48

RESULT 5
 AR093240
 LOCUS AR093240 30 bp DNA linear PAT 08-
 SEP-2000
 DEFINITION Sequence 14 from patent US 5998697.
 ACCESSION AR093240
 VERSION AR093240.1 GI:10019990
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Devlin,R.H.
 TITLE Transgenic fish and vectors therefor
 JOURNAL Patent: US 5998697-A 14 07-DEC-1999;

FEATURES
 source 1..30
 /organism="unknown"

ORIGIN

Query Match 17.8%; Score 16.6; DB 6; Length 49;
 Best Local Similarity 71.0%; Pred. No. 2.6e+05;

Qy 17 ATTCCTGGCTGGGTGACAATGCCCT 39
 Db 7 ATCCAGCTGGATGACAATGACT 29

RESULT 6
 C75763/c
 LOCUS C75763 34 bp DNA linear STS 12-
 FEB-1999
 DEFINITION Homo sapiens STS NIB517, DH PROBE, FORWARD PRIMER, sequence
 tagged
 site.
 ACCESSION C75763
 VERSION C75763.1 GI:3176205
 KEYWORDS STS; DH; Digital hybridization.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Asakawa,S. and Shimizu,N.
 TITLE High-fidelity digital hybridization screening
 JOURNAL Genomics 49 (2), 209-217 (1998)
 MEDLINE 98260670
 PUBMED 9598308
 REFERENCE 2 (bases 1 to 34)
 AUTHORS Asakawa,S. and Shimizu,N.
 TITLE Direct Submission
 JOURNAL Submitted (09-SEP-1997) Shuichi Asakawa, Keio University
 School of Medicine, Department of Molecular Biology; Shinanomachi 35,
 Shinjuku-ku, Tokyo 160, Japan (E-mail:asa@dmbs.med.keio.ac.jp,
 Tel:81-3-3351-2370)

FEATURES
 source 1..34
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 17.8%; Score 16.6; DB 11; Length 34;
 Best Local Similarity 71.0%; Pred. No. 2.5e+05;
 Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 5 TGGGAGCACTCCATTCTGCCCTGGGTGACAAT 35
 Db 31 TGTGAGCTAGTCATTCAAGCTGTGTAACCAT 1

RESULT 7
 I44807/c
 LOCUS I44807 39 bp DNA linear PAT 07-
 OCT-1997
 DEFINITION Sequence 31 from patent US 5635599.
 ACCESSION I44807
 VERSION I44807.1 GI:2469520
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 39)
 AUTHORS Pastan,I.H., Kreitman,R.J. and Puri,R.K.
 TITLE Fusion protein comprising circularly permuted ligands
 JOURNAL Patent: US 5635599-A 31 03-JUN-1997;

FEATURES
 source 1..39
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 17.8%; Score 16.6; DB 6; Length 39;
 Best Local Similarity 71.0%; Pred. No. 2.5e+05;
 Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 43 TTTCACACTATCGGAATGTGACTGTGGC 73
 Db 35 TCTCAACACTCACCGGAGGTAAACGGTGGGGC 5

RESULT 8
 I79331
 LOCUS I79331 49 bp DNA linear PAT 10-
 JUN-1998
 DEFINITION Sequence 34 from patent US 5707796.
 ACCESSION I79331
 VERSION I79331.1 GI:3207621
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 49)
 AUTHORS Gold,L. and Beutel,B.
 TITLE Method for selecting nucleic acids on the basis of structure
 JOURNAL Patent: US 5707796-A 34 13-JAN-1998;

FEATURES
 source 1..49
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 17.8%; Score 16.6; DB 6; Length 49;
 Best Local Similarity 71.0%; Pred. No. 2.6e+05;

Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 49 CACTATGGAAATGTGACTGTGGGCCCTCCAG 79
 ||||| ||| ||| ||| ||| ||| ||| |||
 Db 19 CACTATGGGAGATGCCCTGAGCATGCTG 49

RESULT 9
 AR125663 LOCUS AR125663 50 bp DNA linear PAT 16-
 MAY-2001
 DEFINITION Sequence 5 from patent US 6177557.
 ACCESSION AR125663
 VERSION AR125663.1 GI:14111725
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Janjic,N., Gold,L. and Tasset,D.
 TITLE High affinity ligands of basic fibroblast growth factor and thrombin.
 JOURNAL Patent: US 6177557-A 5 23-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..50
 /organism="unknown"
 /mol_type="unassigned DNA"
 ORIGIN
 Query Match 17.8%; Score 16.6; DB 6; Length 50;
 Best Local Similarity 71.0%; Pred. No. 2.6e+05;
 Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 49 CACTATGGAAATGTGACTGTGGGCCCTCCAG 79
 ||||| ||| ||| ||| ||| ||| ||| |||
 Db 20 CACTATGGGAGATGCCCTGAGCATGCTG 50

RESULT 10
 I47075 LOCUS I47075 50 bp DNA linear PAT 07-
 OCT-1997
 DEFINITION Sequence 5 from patent US 5639868.
 ACCESSION I47075
 VERSION I47075.1 GI:2471040
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Janjic,N. and Gold,L.
 TITLE High-affinity RNA ligands for basic fibroblast growth factor
 JOURNAL Patent: US 5639868-A 5 17-JUN-1997;
 FEATURES Location/Qualifiers
 source 1..50
 /organism="unknown"
 /mol_type="unassigned DNA"
 ORIGIN
 Query Match 17.8%; Score 16.6; DB 6; Length 50;
 Best Local Similarity 71.0%; Pred. No. 2.6e+05;
 Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 49 CACTATGGAAATGTGACTGTGGGCCCTCCAG 79
 ||||| ||| ||| ||| ||| ||| |||
 Db 20 CACTATGGGAGATGCCCTGAGCATGCTG 50

RESULT 11
 AR149818/c LOCUS AR149818 47 bp DNA linear PAT 08-
 AUG-2001
 DEFINITION Sequence 19 from patent US 6228621.
 ACCESSION AR149818
 VERSION AR149818.1 GI:15114409
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 47)
 AUTHORS Williams,W.V., Madaio,M. and Weiner,D.B.
 TITLE Plasmids encoding immunogenic proteins and intracellular targeting sequences
 JOURNAL Patent: US 6228621-A 19 08-MAY-2001;
 FEATURES Location/Qualifiers
 source 1..47
 /organism="unknown"
 /mol_type="unassigned DNA"
 ORIGIN
 Query Match 17.6%; Score 16.4; DB 6; Length 47;
 Best Local Similarity 60.5%; Pred. No. 3.1e+05;
 Matches 23; Conservative 2; Mismatches 13; Indels 0; Gaps 0;
 Qy 55 CGGAATGTGACTGTGGGCCCTCCAGAAAATGGGT 92
 |||:||| ||| ||| ||| ||| ||| |||
 Db 46 CAGRYTGYTGAGCTGGACCTCCTGATAAGATTTAGAT 9

RESULT 12
 AR289717/c LOCUS AR289717 47 bp DNA linear PAT 12-
 JUN-2003
 DEFINITION Sequence 1452 from patent US 6537751.
 ACCESSION AR289717
 VERSION AR289717.1 GI:31677001
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 47)
 AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
 TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
 JOURNAL Patent: US 6537751-A 1452 25-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..47
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN
 Query Match 17.6%; Score 16.4; DB 6; Length 47;
 Best Local Similarity 67.6%; Pred. No. 3.1e+05;
 Matches 23; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 Qy 20 CTGCTTGGGTGACAATGCCCTGGTTCAACACTA 53
 |||:||| ||| ||| ||| ||| |||
 Db 36 CTGCTTCCCTACRTAATGCCCTGGTTCCATCCTA 3

RESULT 13
 BD007169/c LOCUS BD007169 47 bp DNA linear PAT 31-
 JAN-2002
 DEFINITION Improved vaccines.
 ACCESSION BD007169
 VERSION BD007169.1 GI:18635540
 KEYWORDS JP 2001053260-A/14.
 SOURCE unidentified
 ORGANISM unidentified
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 47)
 AUTHORS Williams,W.V., Madaio,M. and Wehner,D.B.
 TITLE Improved vaccines
 JOURNAL Patent: JP 2001053260-A 14 13-MAR-2001;
 THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
 COMMENT OS Unknown
 PN JP 2001053260-A/14
 PD 13-MAR-2001
 PP 23-OCT-1997 JP 1998519728
 PR 23-OCT-1996 US 60/029592
 PI WILLIAM V WILLIAMS, MICHAEL MADAIO, DAVID B WEHNER PC
 C12N15/09, A61K48/00//A61K39/00, C12N15/00
 CC
 FH Key Location/Qualifiers
 FT source 1..47
 FT /organism="Unknown".
 FEATURES Location/Qualifiers
 source 1..47
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"
 ORIGIN
 Query Match 17.6%; Score 16.4; DB 6; Length 47;
 Best Local Similarity 60.5%; Pred. No. 3.1e+05;
 Matches 23; Conservative 2; Mismatches 13; Indels 0; Gaps 0;
 Qy 55 CGGAATGTGACTGTGGGCCCTCCAGAAAATGGGT 92
 |||:||| ||| ||| ||| ||| |||
 Db 46 CAGRYTGYTGAGCTGGACCTCCTGATAAGATTTAGAT 9

RESULT 14
 AX159152 LOCUS AX159152 50 bp DNA linear PAT 22-
 JUN-2001
 DEFINITION Sequence 2480 from Patent WO0140521.
 ACCESSION AX159152
 VERSION AX159152.1 GI:14540483
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shimkets,R.A. and Leach,M.
 TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
 JOURNAL Patent: WO 0140521-A 2480 07-JUN-2001;
 Curagen Corporation (US)
 FEATURES Location/Qualifiers
 source 1..50
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 misc_feature 25..26
 /note="Nucleotide deleted between bases 25 and 26
 Accession number cg39667412"
 misc_feature 26
 /note="# of 2 allelic variants (2479 is other entry)"
 ORIGIN
 Query Match 17.6%; Score 16.4; DB 6; Length 50;
 Best Local Similarity 61.9%; Pred. No. 3.2e+05;
 Matches 26; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
 Qy 37 CCTTGGTTCAACACTATCGGAATGTGACTGTGGCCCTCA 78
 |||:||| ||| ||| ||| ||| ||| |||
 Db 9 CCATGGGTGACACAGGGGACTGTCATCACAGGCTTCA 50

RESULT 15
 AR078049/c LOCUS AR078049 40 bp DNA linear PAT 31-
 AUG-2000
 DEFINITION Sequence 103 from patent US 5962272.
 ACCESSION AR078049
 VERSION AR078049.1 GI:10004795